

RAW SEQUENCE LISTING

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Application Serial Number: 09/747, S21A
Source: IFW16
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IFW16

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DATE: 11/09/2006

PATENT APPLICATION: US/09/747,521A

TIME: 10:22:49

Input Set : N:\efs\09747521a_efs\sequen1.txt

Output Set: N:\CRF4\11092006\I747521A.raw

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3 <110> APPLICANT: GALLOWAY, DARREL R.
4 MATECZUN, ALFRED J.
6 <120> TITLE OF INVENTION: METHODS FOR PROTECTION AGAINST LETHAL INFECTION, WITH
7 BACILLUS ANTHRACIS
9 <130> FILE REFERENCE: 22727-04079
11 <140> CURRENT APPLICATION NUMBER: 09/747,521A
12 <141> CURRENT FILING DATE: 2000-12-21
14 <150> PRIOR APPLICATION NUMBER: 60/171,459
15 <151> PRIOR FILING DATE: 1999-12-22
17 <160> NUMBER OF SEQ ID NOS: 10
19 <170> SOFTWARE: PatentIn Ver. 3.3
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2430
23 <212> TYPE: DNA
24 <213> ORGANISM: Bacillus anthracis
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)..(2427)
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32 Met Asn Ile Lys Lys Glu Phe Ile Lys Val Ile Ser Met Ser Cys Leu
33 1 5 10 15
35 gta aca gca att act ttg agt ggt ccc gtc ttt atc ccc ctt gta cag 96
36 Val Thr Ala Ile Thr Leu Ser Gly Pro Val Phe Ile Pro Leu Val Gln
37 20 25 30
39 ggg gcg ggc ggt cat ggt gat gta ggt atg cac gta aaa gag aaa gag 144
40 Gly Ala Gly Gly His Gly Asp Val Gly Met His Val Lys Glu Lys Glu
41 35 40 45
43 aaa aat aaa gat gag aat aag aga aaa gat gaa gaa cga aat aaa aca 192
44 Lys Asn Lys Asp Glu Asn Lys Arg Lys Asp Glu Glu Arg Asn Lys Thr
45 50 55 60
47 cag gaa gag cat tta aag gaa atc atg aaa cac att gta aaa ata gaa 240
48 Gln Glu Glu His Leu Lys Glu Ile Met Lys His Ile Val Lys Ile Glu
49 65 70 75 80
51 gta aaa ggg gag gaa gct gtt aaa aaa gag gca gca gaa aag cta ctt 288
52 Val Lys Gly Glu Glu Ala Val Lys Lys Glu Ala Ala Glu Lys Leu Leu
53 85 90 95
55 gag aaa gta cca tct gat gtt tta gag atg tat aaa gca att gga gga 336
56 Glu Lys Val Pro Ser Asp Val Leu Glu Met Tyr Lys Ala Ile Gly Gly
57 100 105 110
59 aag ata tat att gtg gat ggt gat att aca aaa cat ata tct tta gaa 384
60 Lys Ile Tyr Ile Val Asp Gly Asp Ile Thr Lys His Ile Ser Leu Glu
61 115 120 125

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63 gca tta tct gaa gat aag aaa aaa ata aaa gac att tat ggg aaa gat 432
64 Ala Leu Ser Glu Asp Lys Lys Lys Ile Lys Asp Ile Tyr Gly Lys Asp
65 130 135 140
67 gct tta tta cat gaa cat tat gta tat gca aaa gaa gga tat gaa ccc 480
68 Ala Leu Leu His Glu His Tyr Val Tyr Ala Lys Glu Gly Tyr Glu Pro
69 145 150 155 160
71 gta ctt gta atc caa tct tcg gaa gat tat gta gaa aat act gaa aag 528
72 Val Leu Val Ile Gln Ser Ser Glu Asp Tyr Val Glu Asn Thr Glu Lys
73 165 170 175
75 gca ctg aac gtt tat tat gaa ata ggt aag ata tta tca agg gat att 576
76 Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys Ile Leu Ser Arg Asp Ile
77 180 185 190
79 tta agt aaa att aat caa cca tat cag aaa ttt tta gat gta tta aat 624
80 Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys Phe Leu Asp Val Leu Asn
81 195 200 205
83 acc att aaa aat gca tct gat tca gat gga caa gat ctt tta ttt act 672
84 Thr Ile Lys Asn Ala Ser Asp Ser Asp Gly Gln Asp Leu Leu Phe Thr
85 210 215 220
87 aat cag ctt aag gaa cat ccc aca gac ttt tct gta gaa ttc ttg gaa 720
88 Asn Gln Leu Lys Glu His Pro Thr Asp Phe Ser Val Glu Phe Leu Glu
89 225 230 235 240
91 caa aat agc aat gag gta caa gaa gta ttt gcg aaa gct ttt gca tat 768
92 Gln Asn Ser Asn Glu Val Gln Glu Val Phe Ala Lys Ala Phe Ala Tyr
93 245 250 255
95 tat atc gag cca cag cat cgt gat gtt tta cag ctt tat gca ccg gaa 816
96 Tyr Ile Glu Pro Gln His Arg Asp Val Leu Gln Leu Tyr Ala Pro Glu
97 260 265 270
99 gct ttt aat tac atg gat aaa ttt aac gaa caa gaa ata aat cta tcc 864
100 Ala Phe Asn Tyr Met Asp Lys Phe Asn Glu Gln Glu Ile Asn Leu Ser
101 275 280 285
103 ttg gaa gaa ctt aaa gat caa cgg atg ctg tca aga tat gaa aaa tgg 912
104 Leu Glu Glu Leu Lys Asp Gln Arg Met Leu Ser Arg Tyr Glu Lys Trp
105 290 295 300
107 gaa aag ata aaa cag cac tat caa cac tgg agc gat tct tta tct gaa 960
108 Glu Lys Ile Lys Gln His Tyr Gln His Trp Ser Asp Ser Leu Ser Glu
109 305 310 315 320
111 gaa gga aga gga ctt tta aaa aag ctg cag att cct att gag cca aag 1008
112 Glu Gly Arg Gly Leu Leu Lys Lys Leu Gln Ile Pro Ile Glu Pro Lys
113 325 330 335
115 aaa gat gac ata att cat tct tta tct caa gaa gaa aaa gag ctt cta 1056
116 Lys Asp Asp Ile Ile His Ser Leu Ser Gln Glu Glu Lys Glu Leu Leu
117 340 345 350
119 aaa aga ata caa att gat agt agt gat ttt tta tct act gag gaa aaa 1104
120 Lys Arg Ile Gln Ile Asp Ser Ser Asp Phe Leu Ser Thr Glu Glu Lys
121 355 360 365
123 gag ttt tta aaa aag cta caa att gat att cgt gat tct tta tct gaa 1152
124 Glu Phe Leu Lys Lys Leu Gln Ile Asp Ile Arg Asp Ser Leu Ser Glu
125 370 375 380
127 gaa gaa aaa gag ctt tta aat aga ata cag gtg gat agt agt aat cct 1200

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128	Glu	Glu	Lys	Glu	Leu	Leu	Asn	Arg	Ile	Gln	Val	Asp	Ser	Ser	Asn	Pro	
129	385					390					395					400	
131	tta	tct	gaa	aaa	gaa	aaa	gag	ttt	tta	aaa	aag	ctg	aaa	ctt	gat	att	1248
132	Leu	Ser	Glu	Lys	Glu	Lys	Glu	Phe	Leu	Lys	Lys	Leu	Lys	Leu	Asp	Ile	
133					405					410						415	
135	caa	cca	tat	gat	att	aat	caa	agg	ttg	caa	gat	aca	gga	ggg	tta	att	1296
136	Gln	Pro	Tyr	Asp	Ile	Asn	Gln	Arg	Leu	Gln	Asp	Thr	Gly	Gly	Leu	Ile	
137				420					425						430		
139	gat	agt	ccg	tca	att	aat	ctt	gat	gta	aga	aag	cag	tat	aaa	agg	gat	1344
140	Asp	Ser	Pro	Ser	Ile	Asn	Leu	Asp	Val	Arg	Lys	Gln	Tyr	Lys	Arg	Asp	
141			435					440						445			
143	att	caa	aat	att	gat	gct	tta	tta	cat	caa	tcc	att	gga	agt	acc	ttg	1392
144	Ile	Gln	Asn	Ile	Asp	Ala	Leu	Leu	His	Gln	Ser	Ile	Gly	Ser	Thr	Leu	
145		450					455					460					
147	tac	aat	aaa	att	tat	ttg	tat	gaa	aat	atg	aat	atc	aat	aac	ctt	aca	1440
148	Tyr	Asn	Lys	Ile	Tyr	Leu	Tyr	Glu	Asn	Met	Asn	Ile	Asn	Asn	Leu	Thr	
149	465					470					475					480	
151	gca	acc	cta	ggg	gcg	gat	tta	ggt	gat	tcc	act	gat	aat	act	aaa	att	1488
152	Ala	Thr	Leu	Gly	Ala	Asp	Leu	Val	Asp	Ser	Thr	Asp	Asn	Thr	Lys	Ile	
153				485						490					495		
155	aat	aga	ggg	att	ttc	aat	gaa	ttc	aaa	aaa	aat	ttc	aaa	tat	agt	att	1536
156	Asn	Arg	Gly	Ile	Phe	Asn	Glu	Phe	Lys	Lys	Asn	Phe	Lys	Tyr	Ser	Ile	
157			500						505					510			
159	tct	agt	aac	tat	atg	att	ggt	gat	ata	aat	gaa	agg	cct	gca	tta	gat	1584
160	Ser	Ser	Asn	Tyr	Met	Ile	Val	Asp	Ile	Asn	Glu	Arg	Pro	Ala	Leu	Asp	
161			515					520					525				
163	aat	gag	cgt	ttg	aaa	tgg	aga	atc	caa	tta	tca	cca	gat	act	cga	gca	1632
164	Asn	Glu	Arg	Leu	Lys	Trp	Arg	Ile	Gln	Leu	Ser	Pro	Asp	Thr	Arg	Ala	
165		530					535					540					
167	gga	tat	tta	gaa	aat	gga	aag	ctt	ata	tta	caa	aga	aac	atc	ggg	ctg	1680
168	Gly	Tyr	Leu	Glu	Asn	Gly	Lys	Leu	Ile	Leu	Gln	Arg	Asn	Ile	Gly	Leu	
169	545					550					555					560	
171	gaa	ata	aag	gat	gta	caa	ata	att	aag	caa	tcc	gaa	aaa	gaa	tat	ata	1728
172	Glu	Ile	Lys	Asp	Val	Gln	Ile	Ile	Lys	Gln	Ser	Glu	Lys	Glu	Tyr	Ile	
173				565						570					575		
175	agg	att	gat	gcg	aaa	gta	gtg	cca	aag	agt	aaa	ata	gat	aca	aaa	att	1776
176	Arg	Ile	Asp	Ala	Lys	Val	Val	Pro	Lys	Ser	Lys	Ile	Asp	Thr	Lys	Ile	
177			580						585					590			
179	caa	gaa	gca	cag	tta	aat	ata	aat	cag	gaa	tgg	aat	aaa	gca	tta	ggg	1824
180	Gln	Glu	Ala	Gln	Leu	Asn	Ile	Asn	Gln	Glu	Trp	Asn	Lys	Ala	Leu	Gly	
181			595					600						605			
183	tta	cca	aaa	tat	aca	aag	ctt	att	aca	ttc	aac	gtg	cat	aat	aga	tat	1872
184	Leu	Pro	Lys	Tyr	Thr	Lys	Leu	Ile	Thr	Phe	Asn	Val	His	Asn	Arg	Tyr	
185		610					615					620					
187	gca	tcc	aat	att	gta	gaa	agt	gct	tat	tta	ata	ttg	aat	gaa	tgg	aaa	1920
188	Ala	Ser	Asn	Ile	Val	Glu	Ser	Ala	Tyr	Leu	Ile	Leu	Asn	Glu	Trp	Lys	
189	625					630					635					640	
191	aat	aat	att	caa	agt	gat	ctt	ata	aaa	aag	gta	aca	aat	tac	tta	gtt	1968
192	Asn	Asn	Ile	Gln	Ser	Asp	Leu	Ile	Lys	Lys	Val	Thr	Asn	Tyr	Leu	Val	

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193          645          650          655
195 gat ggt aat gga aga ttt gtt ttt acc gat att act ctc cct aat ata 2016
196 Asp Gly Asn Gly Arg Phe Val Phe Thr Asp Ile Thr Leu Pro Asn Ile
197          660          665          670
199 gct gaa caa tat aca cat caa gat gag ata tat gag caa gtt cat tca 2064
200 Ala Glu Gln Tyr Thr His Gln Asp Glu Ile Tyr Glu Gln Val His Ser
201          675          680          685
203 aaa ggg tta tat gtt cca gaa tcc cgt tct ata tta ctc cat gga cct 2112
204 Lys Gly Leu Tyr Val Pro Glu Ser Arg Ser Ile Leu Leu His Gly Pro
205          690          695          700
207 tca aaa ggt gta gaa tta agg aat gat agt gag ggt ttt ata cac gaa 2160
208 Ser Lys Gly Val Glu Leu Arg Asn Asp Ser Glu Gly Phe Ile His Glu
209 705          710          715          720
211 ttt gga cat gct gtg gat gat tat gct gga tat cta tta gat aag aac 2208
212 Phe Gly His Ala Val Asp Asp Tyr Ala Gly Tyr Leu Leu Asp Lys Asn
213          725          730          735
215 caa tct gat tta gtt aca aat tct aaa aaa ttc att gat att ttt aag 2256
216 Gln Ser Asp Leu Val Thr Asn Ser Lys Lys Phe Ile Asp Ile Phe Lys
217          740          745          750
219 gaa gaa ggg agt aat tta act tcg tat ggg aga aca aat gaa gcg gaa 2304
220 Glu Glu Gly Ser Asn Leu Thr Ser Tyr Gly Arg Thr Asn Glu Ala Glu
221          755          760          765
223 ttt ttt gca gaa gcc ttt agg tta atg cat tct acg gac cat gct gaa 2352
224 Phe Phe Ala Glu Ala Phe Arg Leu Met His Ser Thr Asp His Ala Glu
225          770          775          780
227 cgt tta aaa gtt caa aaa aat gct ccg aaa act ttc caa ttt att aac 2400
228 Arg Leu Lys Val Gln Lys Asn Ala Pro Lys Thr Phe Gln Phe Ile Asn
229 785          790          795          800
231 gat cag att aag ttc att att aac tca taa 2430
232 Asp Gln Ile Lys Phe Ile Ile Asn Ser
233          805
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237 <211> LENGTH: 809
238 <212> TYPE: PRT
239 <213> ORGANISM: Bacillus anthracis
241 <400> SEQUENCE: 2
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245 Val Thr Ala Ile Thr Leu Ser Gly Pro Val Phe Ile Pro Leu Val Gln
246 20 25 30
248 Gly Ala Gly Gly His Gly Asp Val Gly Met His Val Lys Glu Lys Glu
249 35 40 45
251 Lys Asn Lys Asp Glu Asn Lys Arg Lys Asp Glu Glu Arg Asn Lys Thr
252 50 55 60
254 Gln Glu Glu His Leu Lys Glu Ile Met Lys His Ile Val Lys Ile Glu
255 65 70 75 80
257 Val Lys Gly Glu Glu Ala Val Lys Lys Glu Ala Ala Glu Lys Leu Leu
258 85 90 95
260 Glu Lys Val Pro Ser Asp Val Leu Glu Met Tyr Lys Ala Ile Gly Gly

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261		100		105		110
263	Lys Ile Tyr	Ile Val Asp Gly Asp	Ile Thr Lys His	Ile Ser Leu Glu		
264		115		120		125
266	Ala Leu Ser	Glu Asp Lys Lys Lys	Ile Lys Asp Ile	Tyr Gly Lys Asp		
267		130		135		140
269	Ala Leu Leu	His Glu His Tyr Val	Tyr Ala Lys Glu	Gly Tyr Glu Pro		
270	145		150		155	160
272	Val Leu Val	Ile Gln Ser Ser Glu	Asp Tyr Val Glu	Asn Thr Glu Lys		
273		165		170		175
275	Ala Leu Asn	Val Tyr Tyr Glu Ile	Gly Lys Ile Leu	Ser Arg Asp Ile		
276		180		185		190
278	Leu Ser Lys	Ile Asn Gln Pro Tyr	Gln Lys Phe Leu	Asp Val Leu Asn		
279		195		200		205
281	Thr Ile Lys	Asn Ala Ser Asp Ser	Asp Gly Gln Asp	Leu Leu Phe Thr		
282		210		215		220
284	Asn Gln Leu	Lys Glu His Pro Thr	Asp Phe Ser Val	Glu Phe Leu Glu		
285	225		230		235	240
287	Gln Asn Ser	Asn Glu Val Gln Glu	Val Phe Ala Lys	Ala Phe Ala Tyr		
288		245		250		255
290	Tyr Ile Glu	Pro Gln His Arg Asp	Val Leu Gln Leu	Tyr Ala Pro Glu		
291		260		265		270
293	Ala Phe Asn	Tyr Met Asp Lys Phe	Asn Glu Gln Glu	Ile Asn Leu Ser		
294		275		280		285
296	Leu Glu Glu	Leu Lys Asp Gln Arg	Met Leu Ser Arg	Tyr Glu Lys Trp		
297		290		295		300
299	Glu Lys Ile	Lys Gln His Tyr Gln	His Trp Ser Asp	Ser Leu Ser Glu		
300	305		310		315	320
302	Glu Gly Arg	Gly Leu Leu Lys Lys	Leu Gln Ile Pro	Ile Glu Pro Lys		
303		325		330		335
305	Lys Asp Asp	Ile Ile His Ser Leu	Ser Gln Glu Glu	Lys Glu Leu Leu		
306		340		345		350
308	Lys Arg Ile	Gln Ile Asp Ser Ser	Asp Phe Leu Ser	Thr Glu Glu Lys		
309		355		360		365
311	Glu Phe Leu	Lys Lys Leu Gln Ile	Asp Ile Arg Asp	Ser Leu Ser Glu		
312		370		375		380
314	Glu Glu Lys	Glu Leu Leu Asn Arg	Ile Gln Val Asp	Ser Ser Asn Pro		
315	385		390		395	400
317	Leu Ser Glu	Lys Glu Lys Glu Phe	Leu Lys Lys Leu	Lys Leu Asp Ile		
318		405		410		415
320	Gln Pro Tyr	Asp Ile Asn Gln Arg	Leu Gln Asp Thr	Gly Gly Leu Ile		
321		420		425		430
323	Asp Ser Pro	Ser Ile Asn Leu Asp	Val Arg Lys Gln	Tyr Lys Arg Asp		
324		435		440		445
326	Ile Gln Asn	Ile Asp Ala Leu Leu	His Gln Ser Ile	Gly Ser Thr Leu		
327		450		455		460
329	Tyr Asn Lys	Ile Tyr Leu Tyr Glu	Asn Met Asn Ile	Asn Asn Leu Thr		
330	465		470		475	480
332	Ala Thr Leu	Gly Ala Asp Leu Val	Asp Ser Thr Asp	Asn Thr Lys Ile		
333		485		490		495

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